

FIGURE 1A

9.1 (SEQ ID NO:1): 5' GGGAGAGAGG AAGAGGGAUG GG CCGCCAGU  
GGGAAGCUAU ACCCAACGCC CCAGCCCCAG AGCAUAACCC AGAGGUCGAU AGUACUGGAU  
CCCCC 3'

9.2 (SEQ ID NO:2): 5' GGGAGAGAGG AAGAGGGAUG GGCUAUAUAC ACGCUGGUGA  
UCCCAUCUCA AUUGAAACAA CACUAACCC AGAGGUCGAU AGUACUGGAU CCCCC 3'

9.3 (SEQ ID NO:3): 5' GGGAGAGAGG AAGAGGGAUG GGGACUAUAC CGCGUAAUGC  
UGCCUCCCCA UCCCGGAACG CUCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCC 3'

9.4 (SEQ ID NO:4): 5' GGGAGAGAGG AAGAGGGAUG GGCACUAUAC GCAUCUUGCU  
GCCUGCCCGC GAGUCAAAU GCAUAACCCA GAGGUCGAU GUACUGGAUC CCCCC 3'

9.5 (SEQ ID NO:5): 5' GGGAGAGAGG AAGAGGGAUG GGCCUACCAG UUCGUGGCUA  
GCGUGACGUA CCACCCAGG ACCUAACCC AGAGGUCGAU AGUACUGGAU CCCCC 3'

9.7 (SEQ ID NO:6): 5' GGGAGAGAGG AAGAGGGAUG GGCGAUAAACC AACAUUGUGA  
UCCCAUUC AUACCCUAC AACUAACCC AGAGGUCGAU AGUACUGGAU CCCCC 3'

9.8 (SEQ ID NO:7): 5' GGGAGAGAGG AAGAGGGAUG GGGCCACC UAUAUACCGGU  
CAUCGUGCAU AGGUCGCGC CACUAACCC AGAGGUCGAU AGUACUGGAU CCCCC 3'

9.9 (SEQ ID NO:8): 5' GGGAGAGAGG AAGAGGGAUG GGUCUCACAC CCGAAGAUGG  
CCAAAGAGG AGAUGAGUUU CCAUAACCCA GAGGUCGAU GUACUGGAUC CCCCC 3'

9.11 (SEQ ID NO:9): 5' GGGAGAGAGG AAGAGGGAUG GGACUAUAUU CGGAUUCUGG  
ACUCCACCU GCCUGCCCCA GACUAACCC AGAGGUCGAU AGUACUGGAU CCCCC 3'

9.12 (SEQ ID NO:10): 5' GGGAGAGAGG AAGAGGGAUG GGCGAUUAUAC  
ACAUUGGUGA UCCACCCAC AUGAAACCAC AGCAUAACCC AGAGGUCGAU AGUACUGGAU  
CCCCC 3'

9.13 (SEQ ID NO:11): 5' GGGAGAGAGG AAGAGGGAUG GGCUCAUCAC  
AGGCGAAGUG AACACACUA CCGNCNAGUU ACCUAACCC AGAGGUCGAU AGUACUGGAU  
CCCCC 3'

9.14 (SEQ ID NO:12): 5' GGGAGAGAGG AAGAGGGAUG GG GACUAUAC  
GUGAACGACU GCAUCCACUUC CCcGCCAUGG CAUAACCCAG AGGUCGAUAG  
UACUGGAUCC CCCC 3'

FIGURE 1A

FIGURE 1B

9.16 (SEQ ID NO:13): 5' GGGAGAGAGG AAGAGGGAUG GGCCAUACGU  
GGACGACUGC ACCCGACCCU UCAGCCCAGG UCCAUAACCC AGAGGUCGAU AGUACUGGAU  
CCCCC 3'

9.17 (SEQ ID NO:14): 5' GGGAGAGAGG AAGAGGGAUG GGACCAUACG  
CACAUUGCUG AAUCCCCcUC AAUAGCACCU ACCAUAAACCC AGAGGUCGAU AGUACUGGAU  
CCCCC 3'

9.18 (SEQ ID NO:15): 5' GGGAGAGAGG AAGAGGGAUG GGCCAUAAAC  
ACUUUGGUGA ACCCACCAG CUCc/UUGUGAU UGCAUAACCC AGAGGUCGAU  
AGUACUGGAU CCCCC 3'

9.19 (SEQ ID NO:16): 5' GGGAGAGAGG AAGAGGGAUG GGACCAUAAC  
GACUACUCGUGA AUCCACCAU CAGCGCACAA CAUAACCCAGA GGUCGAUAG  
UACUGGAUCC CCCC 3'

9.20 (SEQ ID NO:17): 5' GGGAGAGAGG AAGAGGGAUG GGGACUAUAC  
CGGCcAUUCGU GCAUCCCCUG GACCUAACAA UACAUAAACCC AGAGGUCGAU AGUACUGGAU  
CCCCC 3'

9.21 (SEQ ID NO:18): 5' GGGAGAGAGG AAGAGGGAUG GG AACACCAU  
UAAUGCUCGG CCAGGUAACC CCGGCGCAUA CUCAUAACCC AGAGGUCGAU AGUACUGGAU  
CCCCC 3'

9.25 (SEQ ID NO:19): 5' GGGAGAGAGG AAGAGGGAUG GGGACCAUAA  
CUCUAACGGG UGAAUCCCCG AUCUCGACAA UACAUAAACCC AGAGGUCGAU AGUACUGGAU  
CCCCC 3'

9.26 (SEQ ID NO:20): 5' GGGAGAGAGG AAGAGGGAUG GG UGAUAACC  
ACUCUGGUGA ACCCCUCCCG ACUUGCUCGC ACAUAACCCA GAGGUCGAUA GUACUGGAUC  
CCCC 3'

9.27 (SEQ ID NO:21): 5' GGGAGAGAGG AAGAGGGAUG GGUAUAACU  
GUAUGGUGAA CCCACCCAAA CUCCCAUGGC UACAUAAACCC AGAGGUCGAU AGUACUGGAU  
CCCCC 3'

9.28 (SEQ ID NO:22): 5' GGGAGAGAGG AAGAGGGAUG GG CGCCAUAC  
GCACAUUGC U GCAUCGCCU CCCGUAAGAA CCAUAACCCA GAGGUCGAUA GUACUGGAUC  
CCCC 3'

FIGURE 1B

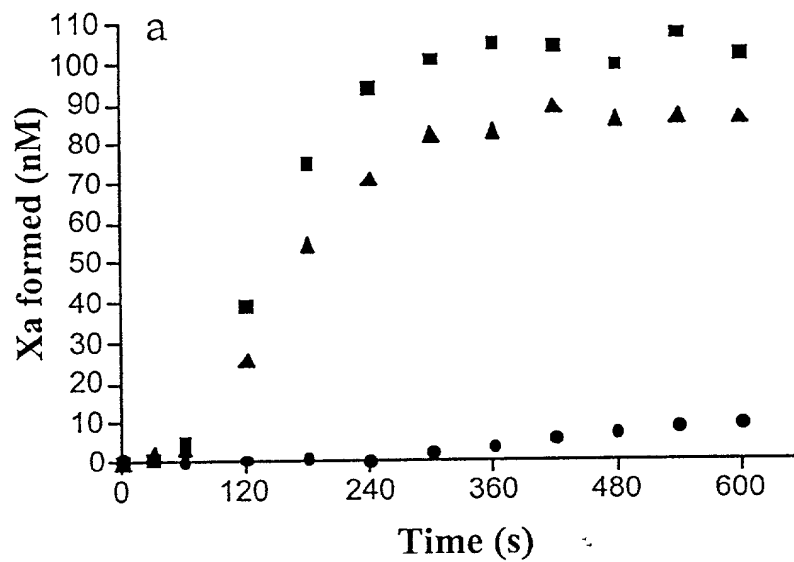
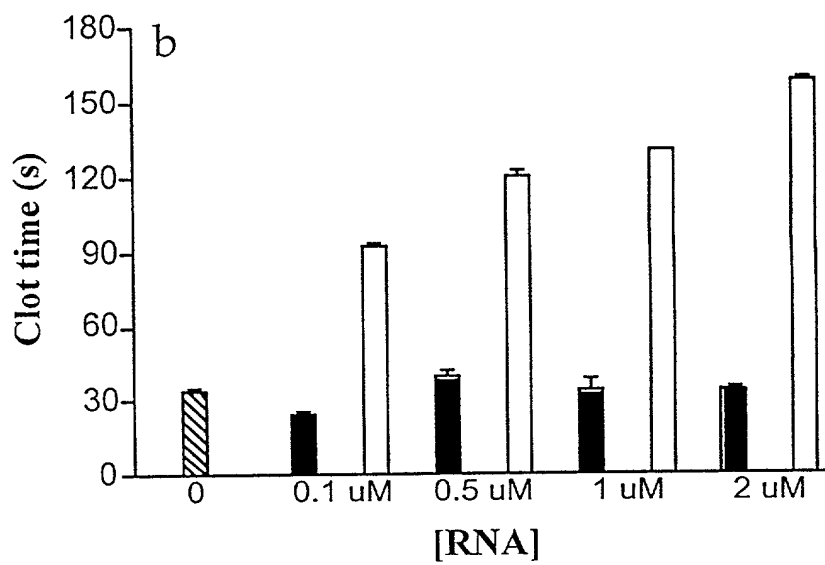


FIGURE 2A

FIGURE 2B



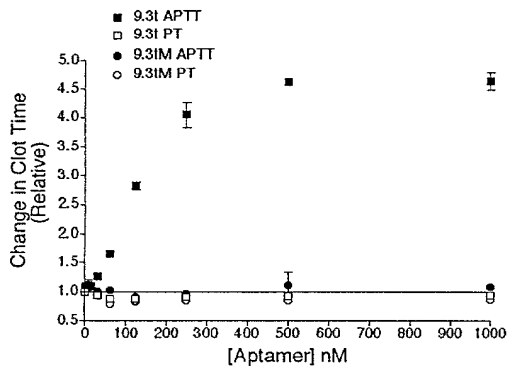


Figure 3A

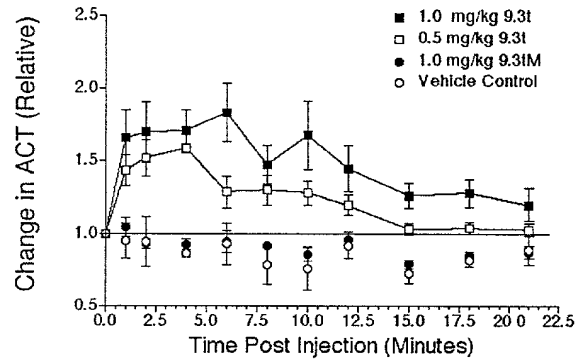


Figure 3B

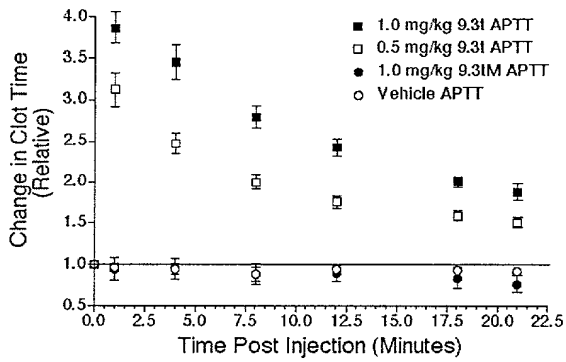


Figure 3C

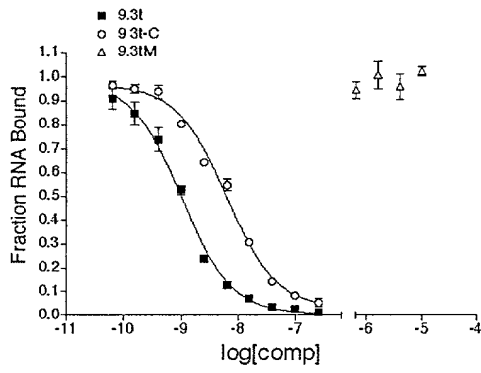


Figure 4A

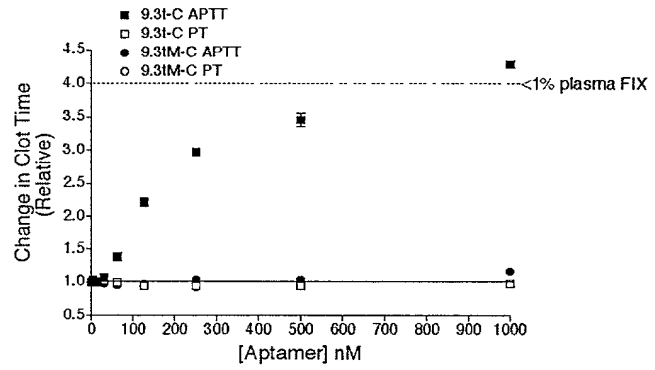


Figure 4B

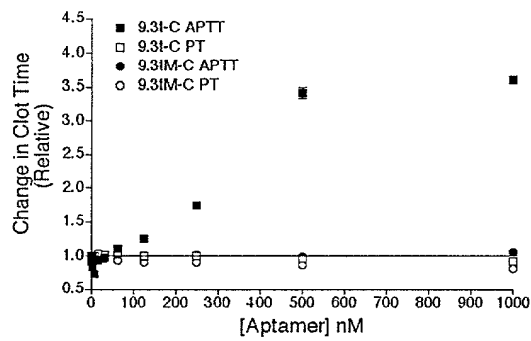


Figure 4C

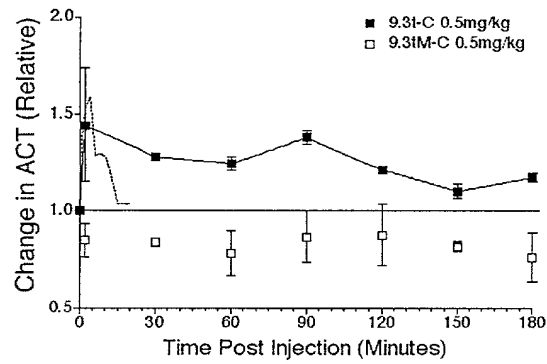


Figure 5A

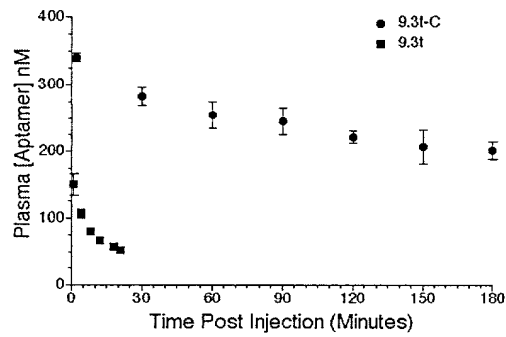


Figure 5B

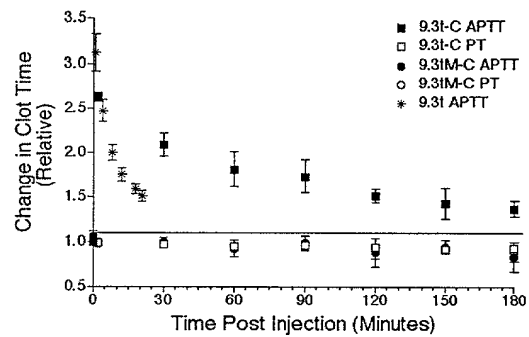


Figure 5C

## Figure 6A

10.1 (SEQ ID NO:23): 5' GGGAGAGAGG AAGAGGGAUG GGAAAAUAGC  
CCCAGCGAGA UAAUACUUGG CCCCCGUACCA CCAUAACCCA GAGGUCGAUA  
GUACUGGAUC CCCC 3'

10.5 (SEQ ID NO:24): 5' GGGAGAGAGG AAGAGGGAUG GGCCAGAAGG  
AACUAAACAC CUGAACCCCC CAUCGCGAGAG ACCAUAACCC AGAGGUCGAU  
AGUACUGGAU CCCCC 3'

10.6 (SEQ ID NO:25): 5' GGGAGAGAGG AAGAGGGAUG GGAUGUCACU  
UGGCCCCUCG CGCACc/aCGCC AGCGAGCCCA UAACCCAGAG GUCGAUAGUA  
CUGGAUCCCC CC 3'

10.7 (SEQ ID NO:26): 5' GGGAGAGAGG AAGAGGGAUG GGACACGCCC  
AGCGAGCUCA AACUUGGCCC CCGUGCAUCA CC CCAUAACC CAGAGGUCGA  
UAGUACUGGA UCCCCC 3'

10.8 (SEQ ID NO:27): 5' GGGAGAGAGG AAGAGGGAUG GGAAGUGCCA  
CAGCGAGCAC AUGACUUGG CCGCAUUGC ACCCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCC 3'

10.11 (SEQ ID NO:28): 5' GGGAGAGAGG AAGAGGGAUG GGAAACUAAU  
GCCCUAGCGA GCAUACCCGG ACUGGCCCCG CCAUAACCC AGAGGUCGAU AGUACUGGAU  
CCCCC 3'

10.12 (SEQ ID NO:29): 5' GGGAGAGAGG AAGAGGGAUG GGAAAAUAGC  
CCCAGCGAGA UAAUACUUGG CCCCUCUACU ACCCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCC 3'

10.13 (SEQ ID NO:30): 5' GGGAGAGAGG AAGAGGGAUG GGCGACCCCA  
CUGGCGGAAA CCGACAAUCA CUCCCCACGA CCAUAACCC AGAGGUCGAU AGUACUGGAU  
CCCCC 3'

10.14 (SEQ ID NO:73): 5' GGGAGAGAGG AAGAGGGAUG GGAAAAUAGC  
CCCAGCGAGA UAAUACUUGG CCCCUCUACU ACCAUAACCC AGAGGUCGAU AGUACUGGAU  
CC 3'

Figure 6B

10.15 (SEQ ID NO:31): 5' GGGAGAGAGG AAGAGGGAUG GGCAGCCCAG  
CGAGGGACAC UUAACCCCCU GUCCCCAUC CAAACCAUA CCCAGAGGUC GAUAGUACUG  
GAUCCCCC 3'

10.18 (SEQ ID NO:32): 5' GGGAGAGAGG AAGAGGGAUG GGCCAGAAGU  
CACCGCGACG GUACUGAACC CCCACCCAA ACCCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCC 3'

10.19 (SEQ ID NO:33): 5' GGGAGAGAGG AAGAGGGAUG GGCCAGAAGU  
GCUCACUACA ACGCUUUGAC CCCCCCAUCC ACAUCCCAUA ACCCAGAGGU CGAUAGUACU  
GGAUCCCCC 3'

10.21 (SEQ ID NO:34): 5' GGGAGAGAGG AAGAGGGAUG GG CCAGCAAC  
CGAAGGGCGG AAUACCCCCC GUCUCCACAU ACCCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCC 3'

10.22 (SEQ ID NO:35): 5' GGGAGAGAGG AAGAGGGAUG GG ACGCGACU  
CAGGCAGCAC UUGACUUGGC CCCUUGCGAU CACCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCC 3'

10.23 (SEQ ID NO:36): 5' GGGAGAGAGG AAGAGGGAUG GG CCAGCAAC  
GCUAACACGG AAUACCCCCC ACCCAACGU GCCCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCC 3'

10.24 (SEQ ID NO:37): 5' GGGAGAGAGG AAGAGGGAUG GG CUUCUCAA  
CCGAAAUACA ACUUUAAAUC AUUUAUCACU UACCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCC 3'

10.30 (SEQ ID NO:38): 5' GGGAGAGAGG AAGAGGGAUG GGAUACGCCG  
AUGCAAGCAU GUCCACACAC CGCAUGCCGU ACCCAUAACC CAGAGGUCGA UAGUACUGGA  
UCCCCC 3'



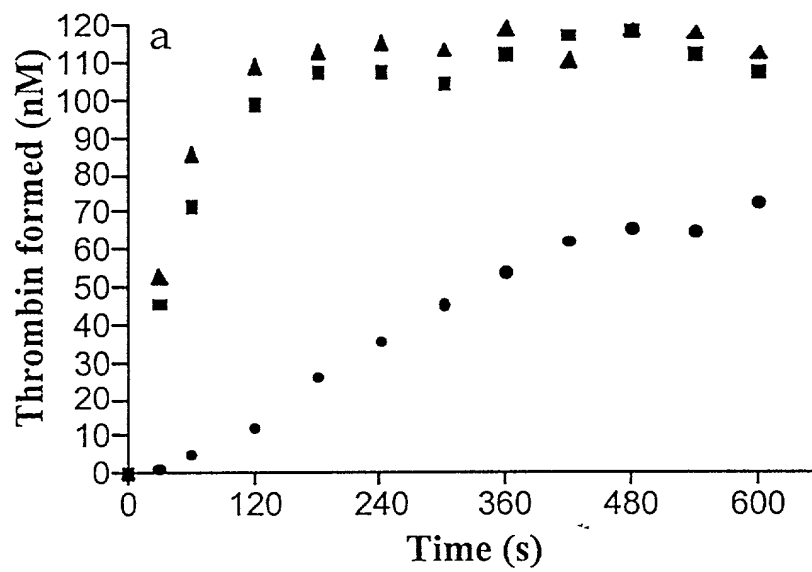
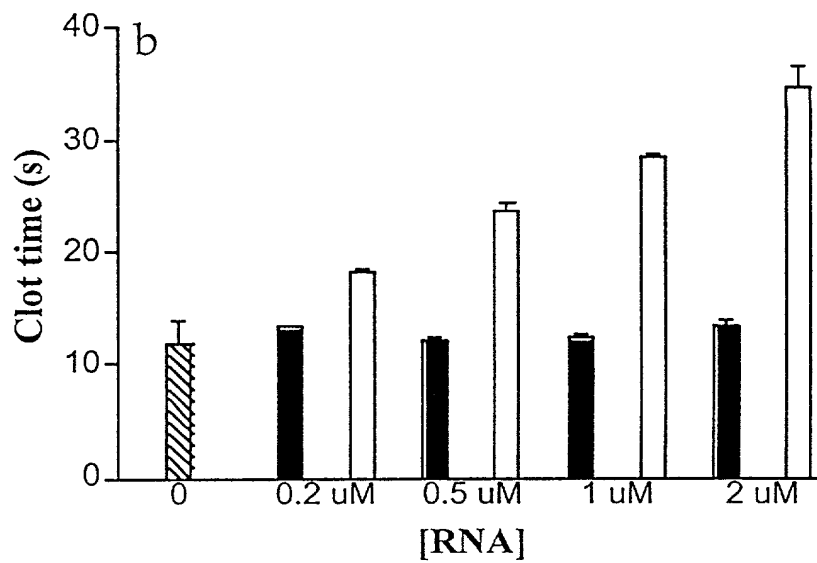


Figure 7A

Figure 7B



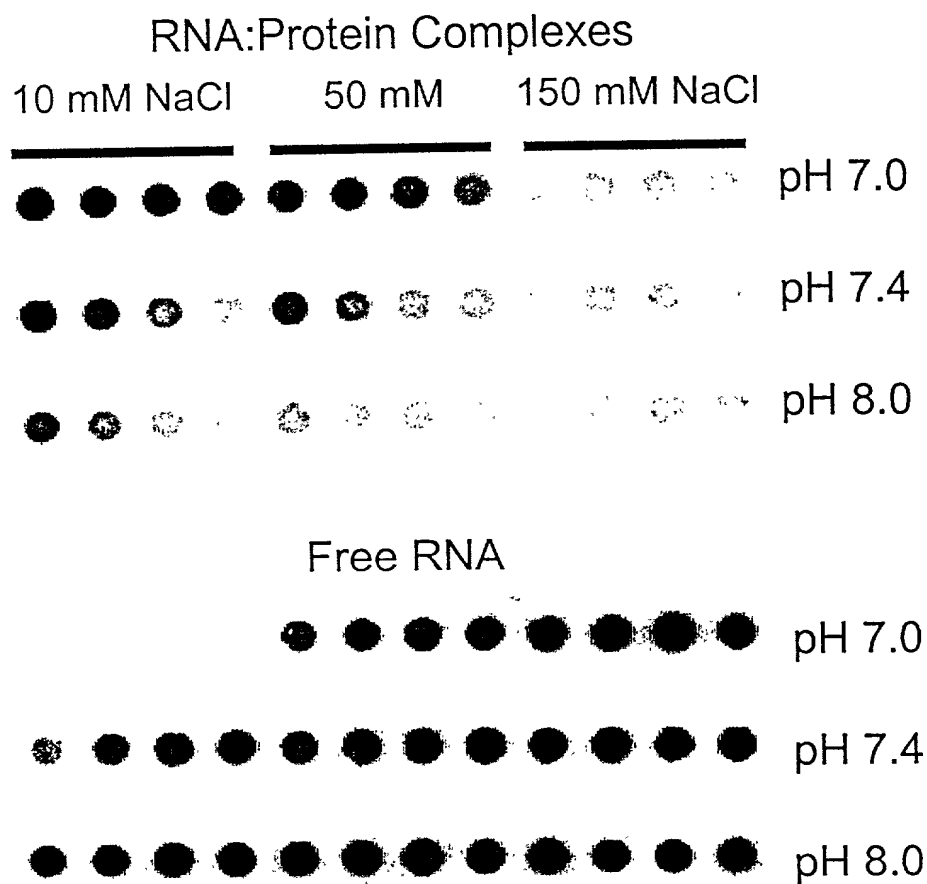
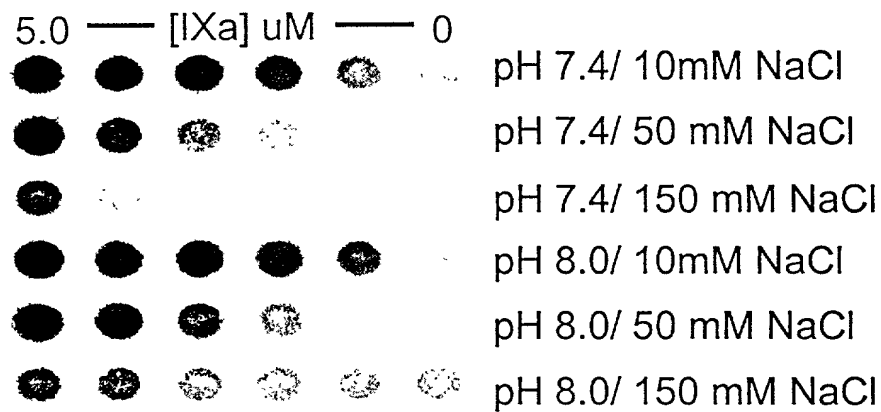


FIGURE 8

10996931-22829660

# RNA:Protein Complexes



# Free RNA

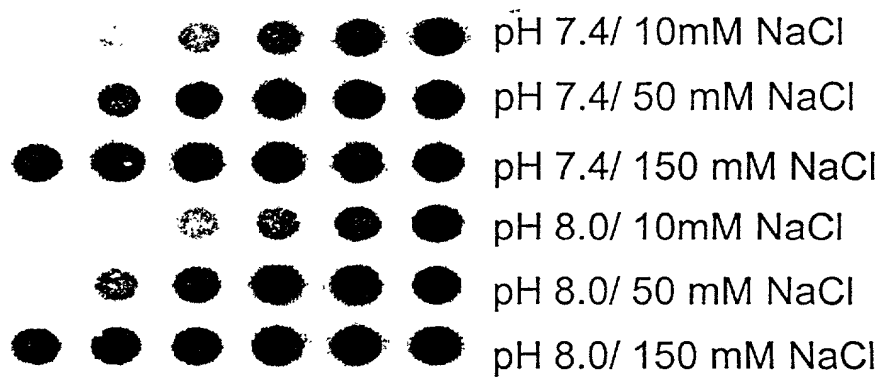


FIGURE 9

Figure 10

16.1: (SEQ ID NO:39) 5' GGGAGAGAGG AAGAGGGAUG GGUACAGAGG AGUACAAGUA  
GCAUGGUCCC CUCGUGUAAA AACAUAAACC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.2 (SEQ ID NO:40): 5' GGGAGAGAGG AAGAGGGAUG GGUGCAAAAG AGCUUCUUGU  
AGUAUGAUCC CUCAACCGCA AGCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.3 (SEQ ID NO:41): 5' GGGAGAGAGG AAGAGGGAUG GG UACAGAGG AGUACAAGUA  
GCAUGAUCCC CUCGUGUAAA AACAUAAACC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.5 (SEQ ID NO:42): 5' GGGAGAGAGG AAGAGGGAUG GGAGCCUAUG UAACAGAUGC  
AGAUCCCUAG UCGUCCCAAC ACCAUAAACC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.7 (SEQ ID NO:43): 5' GGGAGAGAGG AAGAGGGAUG GGCACAACGA ACACCGCAUC  
CCUUGACAGA AAGAGCACGC CUCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.10 (SEQ ID NO:44): 5' GGGAGAGAGG AAGAGGGAUG GGUACAGAGG AGUACAAGUA  
ACAUGAUCCC CUCGUGUAAA AACAUAAACC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.11 (SEQ ID NO:45): 5' GGGAGAGAGG AAGAGGGAUG GG CACAACGA ACACCGCAUC  
CCUUGACAGA AAGAACACGC CUCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

16.18 (SEQ ID NO:46): 5' GGGAGAGAGG AAGAGGGAUG GGCACAAGGA ACACCGCAUC  
CCUUGACAGA AAGAACACGC CUCAUAACCC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

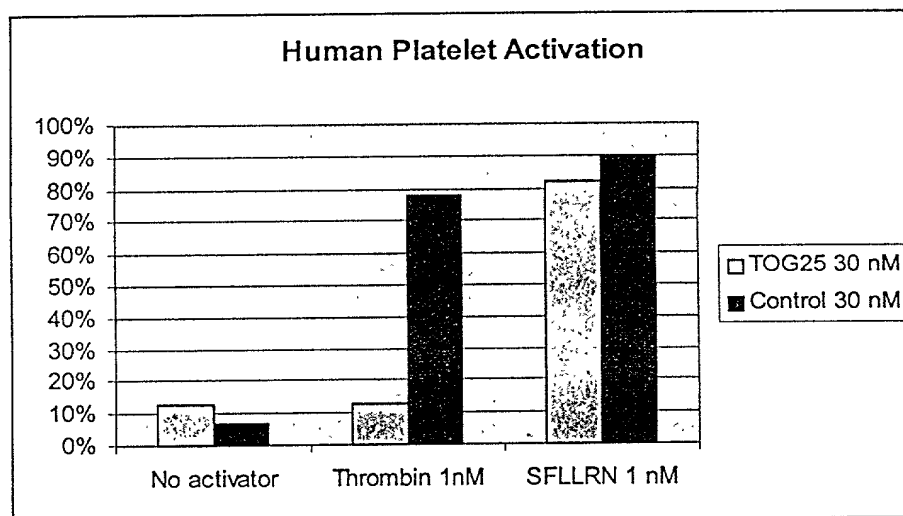
16.20 (SEQ ID NO:47): 5' GGGAGAGAGG AAGAGGGAUG GGAGCCUAUG UAACAGAUGC  
AGAUCCCUAG ACGACCCAAC ACCAUAAACC AGAGGUCGAU AGUACUGGAU CCCCCC 3'

180-228960

FIGURE 11

Random region sequences (Round 13)	K <sub>d</sub> Human Thrombin	K <sub>d</sub> Porcine Thrombin
PIG 5 UGCGAACAAAGCUGAAGUACUUACGCACAACCCGUAGAAU	3 nM	1 nM
PIG 7 AACAAACUGAAGAACUACCCUUCUACUGACGAAUUA	1 nM	<0.5 nM
PIG 8 AAACAAAGCUGAAGUACUUAUCCAUCACCACGCCGAA	1 nM	0.5 nM
PIG 10 UAUUUGGCUUCUCAGUGCCGCAGAGACAGCAACAAUUAGU	>>50 nM	0.5 nM
HUMAN ACAAAGCUGGAGAACUUACCGUCCUCUCCAGAGAUCAA	2 nM	0.5 nM
TOGGLE 25 GAACAAAGCUGAAGUACUUACCCAAGAUAUCCCGAACGA	5 nM	0.5 nM
TOGGLE 30 AACAAAGCUGGAGAACUUAACGUCCUCUCCAGCGGUAA	3 nM	0.5 nM

FIGURE 12



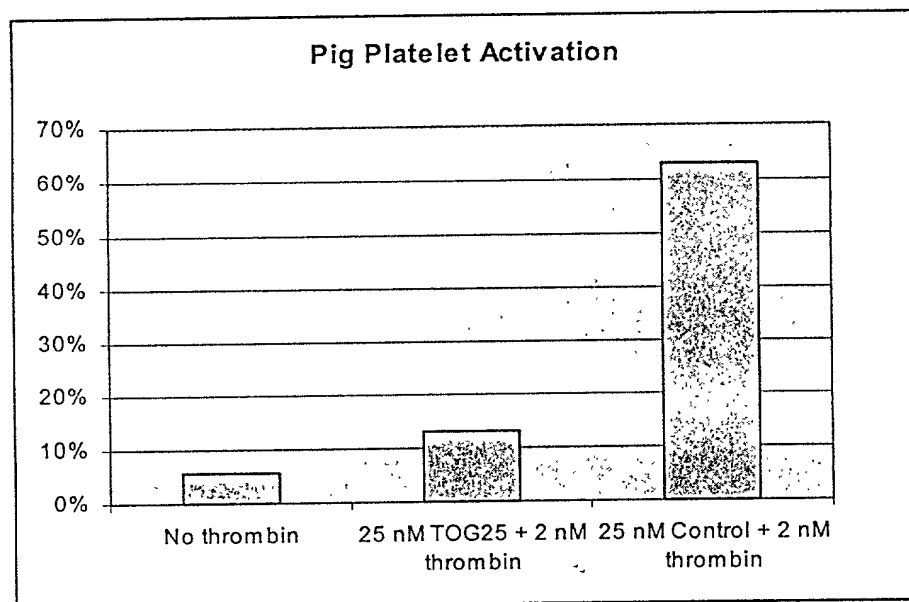


FIGURE 13

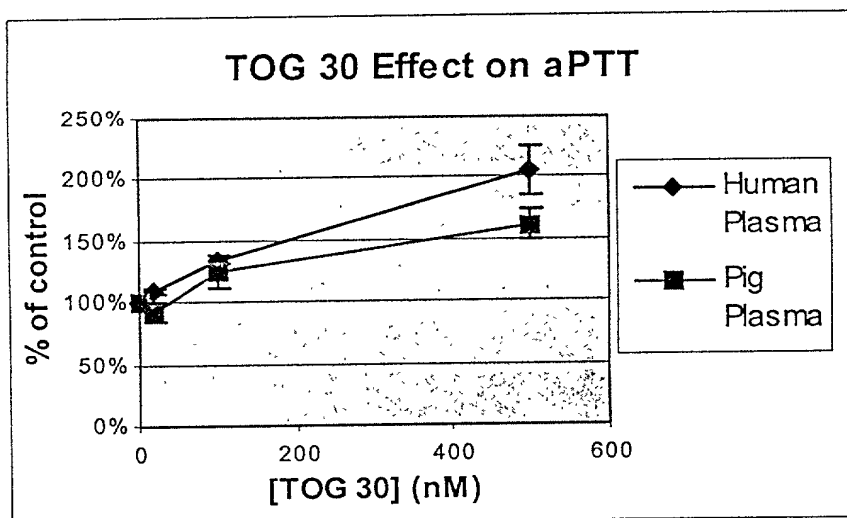


FIGURE 14

Diagram illustrating the RNA hairpin structure and its binding sites. The hairpin consists of a stem (10 base pairs) and a loop (Loop U1,  $K_d \sim 300$  nM). The stem is flanked by two single-stranded regions (NoStem1 and NoStem2) with  $K_d \sim 1000$  nM. The tail (Loop U2,  $K_d \sim 0.5$  nM) is also shown. The sequence of the hairpin is 5'-G-A-A-G-U-C-G-C-A-U-U-A-G-G-G-G-G-3'.

Figure 16

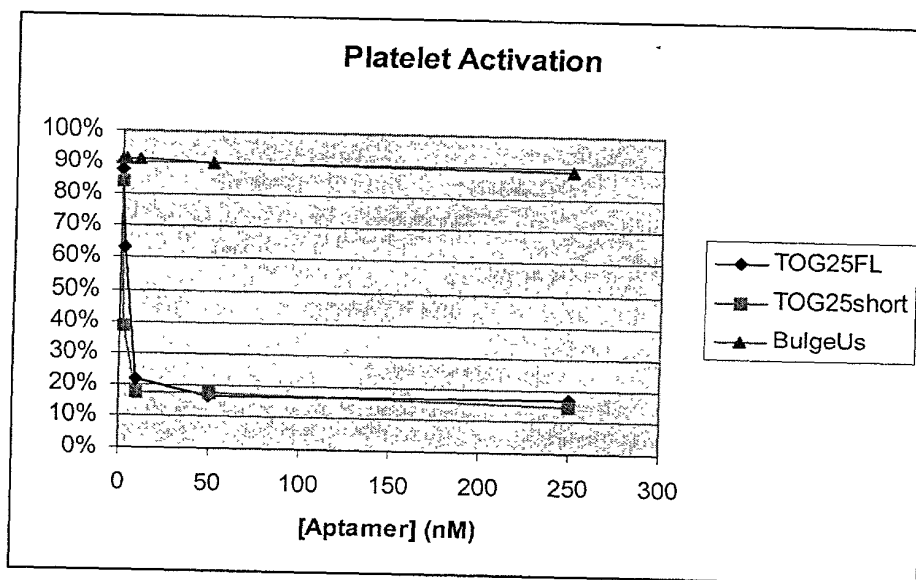




Figure 17

E2F-3 Round 10 Aptamers

5' Primer GGG AGA GAG GAA GAG GGA UGG G (SEQ ID NO: 62)

3' Primer C AUA ACC CAG AGG UCG A A GUA CUG GAUCCC CCC (SEQ ID NO: 63)

10-1 and 10-8 (SEQ ID NO: 64)

5' P-AAUGGA AUC ACUGAA GGC CCUCCG UAG CAC CUA ACA CAGU-3' P

10-2 (SEQ ID NO: 65)

5' P-GCAUCC UGC CAG CGG CGA CGG ACC UC GCC CAC AGG CCUC-3' P

10-3, 10-7, 10-11, and 10-12 (SEQ ID NO: 66)

5' P-UUA UA AGC ACA CUG AAG CCC UCA GCA AAA CCUCCA CAG G-3' P

10-4 (SEQ ID NO: 67)

5' P-UAU GAA AUC ACA GAA GCC CGC GUU CGA CAC CUC CAC UGUU 3' P

10-5 (SEQ ID NO: 68)

5' P-CAA ACUCAC AGA CUC CAA CUG CAG GAG CAC CCA CCC ACA CUG  
GGA CAG-3' P

10-6 (SEQ ID NO: 69)

5' P-AUC CCC GCC GUA AGC CGUCCUGAUGGA CAC CAC ACUCCG C-3' P

103600-2229660

	S1	L1	S2	L2	S2	L3	S1
	→		→		←		←
*9-3 5'	gggaugggGA	CUAUACC	GCG	UAAUGC	UGC	C	UCCCCAUUCC
*9-20 5'	augggGA	CUAUACCG	GCA	AUCG	UGC	A	UCCCCU
*9-25 5'	gggaugggGA	CCAUUA	ACUC	UAAC	GGGU	GAA	UCCCGCAUCU
*9-26 5'	gggauggg	UGAUA	ACCA	CUC	UGGU	GAA	CCCCUCCC
*9-28 5'	gggaugggCG	CCAUAC	GCA	CAU	UGC	UGCAU	CGCCUUCCC
*9-19 5'	gaggggaugggA	CCAUUA	ACGA	CUAC	UCGU	GAA	UCCCACCAUC
9-17 5'	gaggggaugggA	CCAUAC	GCA	CAU	UGC	UGAA	UCCCCCUC
9-11 5'	gggaugggA	CUAUA	UUCGG	AAU	CUGGA		CUCCCACCU
9-4 5'	gggaugggCA	CUAUAC	GCA	UCU	UGC		UGCCUGCCC
9-16 5'	aggggauggg	CCAUUA	CGU	GG	ACG	ACUGCA	CCCGACCCU
9-18 5'	gggauggg	CCAUUA	ACCA	CUU	UGGU	GAA	CCCACCCA
9-7 5'	ggauggg	CGAUA	ACCA	ACA	UGGU	GAU	CCCAUUC
9-12 5'	gggauggg	CGAUA	UAC	ACAUUG	GUG	AU	CCCACCC
9-2 5'	gggauggg	CUAUUA	CAC	GCUG	GUG	AU	CCCAUCUC
9-14 5'	gggaugggGA	CUAUA	CGU	GAACG	ACU	GCA	UCCACUCCCC
9-27 5'	gggauggg	UAAUA	ACU	GUA	UGG	UGAA	CCCACCC

FIGURE 18

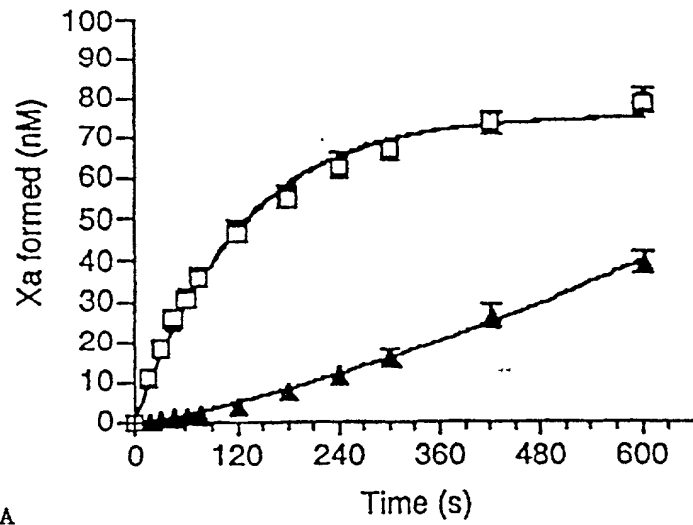


Fig. 19A

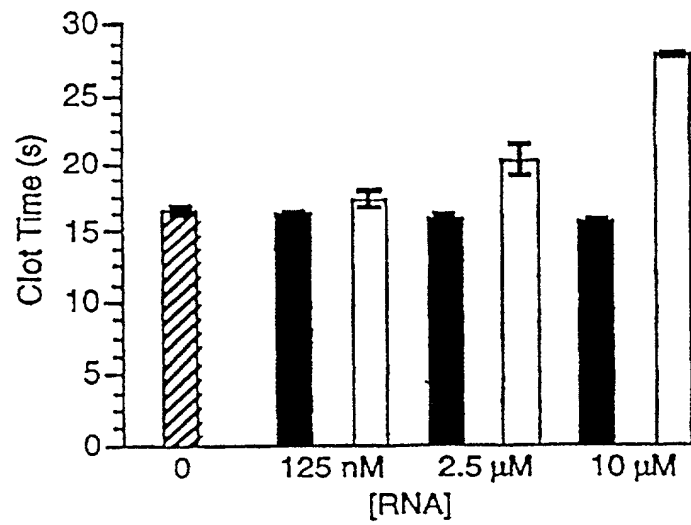


Fig. 19B

Figure 20

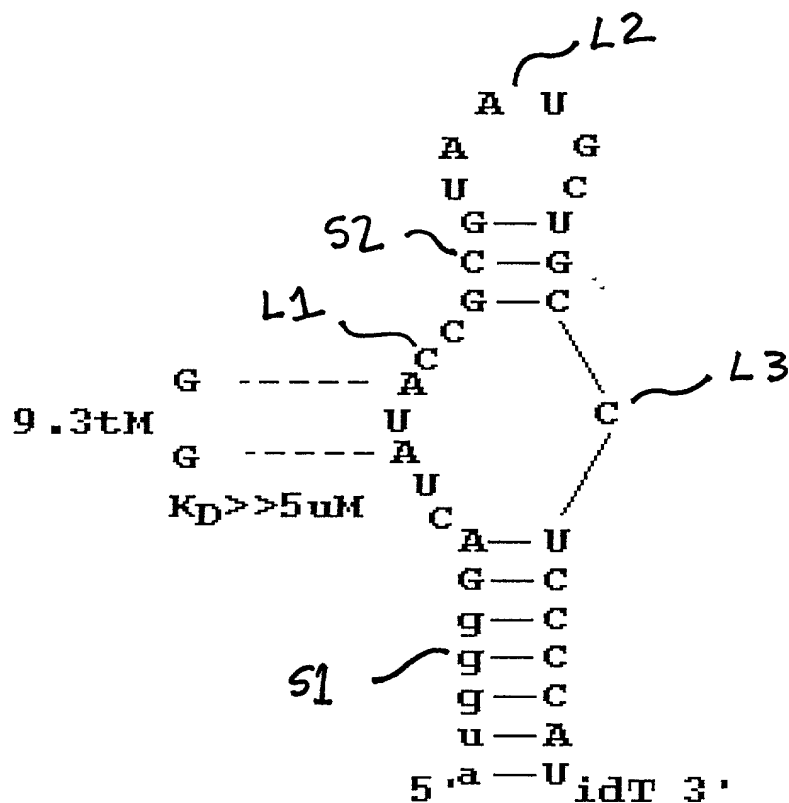
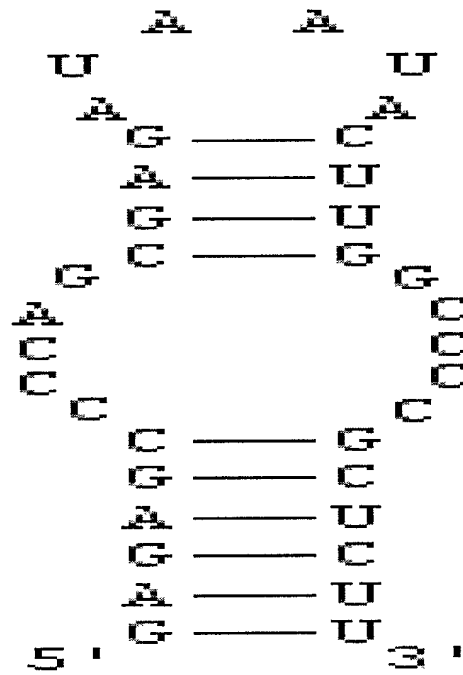


Figure 21



09563927-09504  
T05600-266E9660

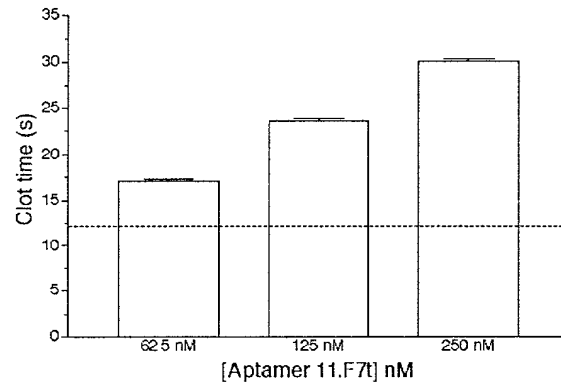


Figure 22A

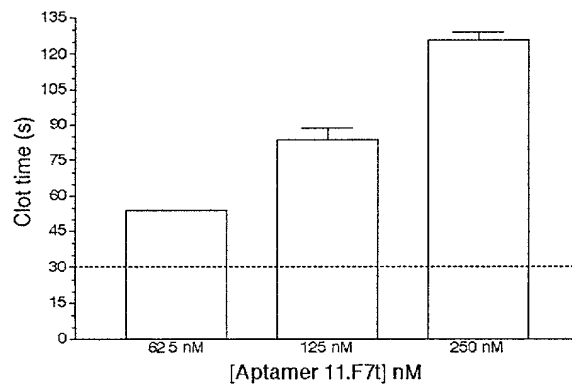


Figure 22B

Figure 23A

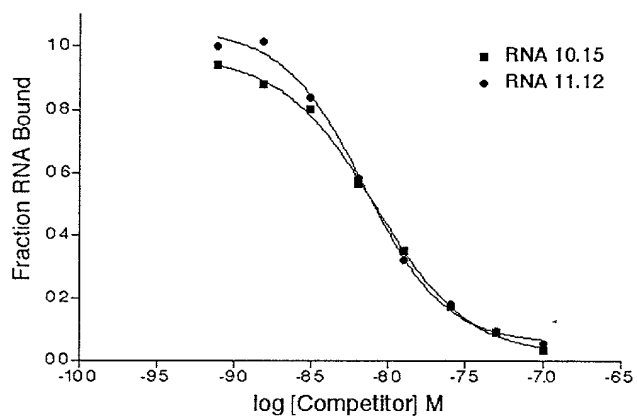


Figure 23B

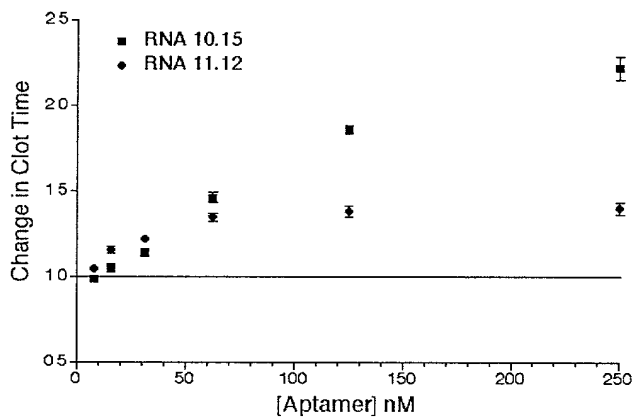


Figure 24

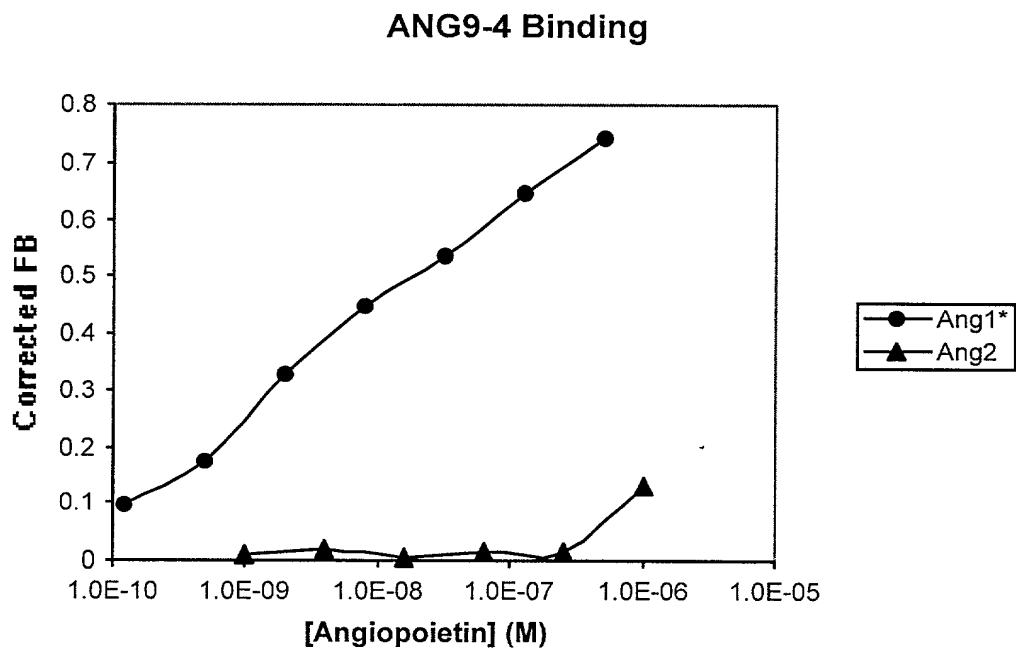
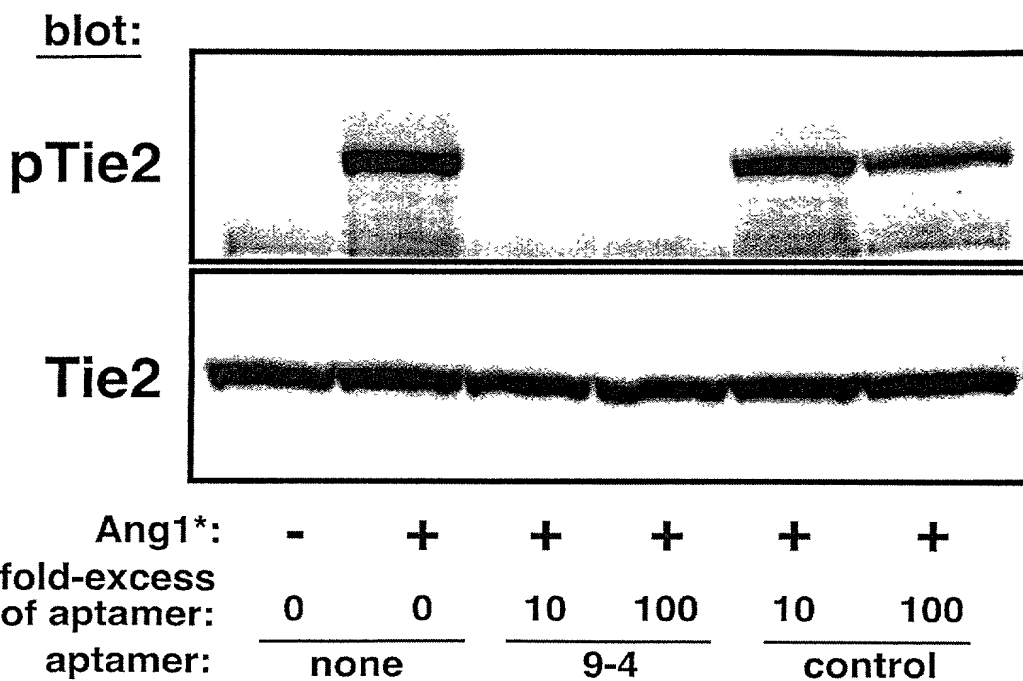
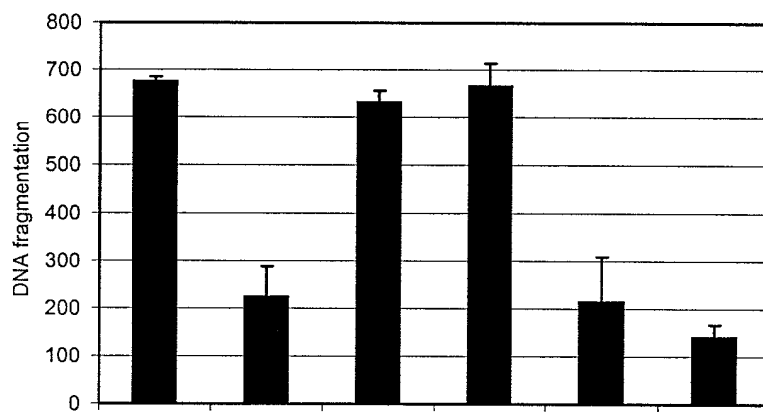


Figure 25







Ang1:	-	+	+	+	+	+
Fold-excess aptamer:	0	0	10	100	10	100
Aptamer:	none		9-4		control	

Figure 26

### ANG11-1 Binding

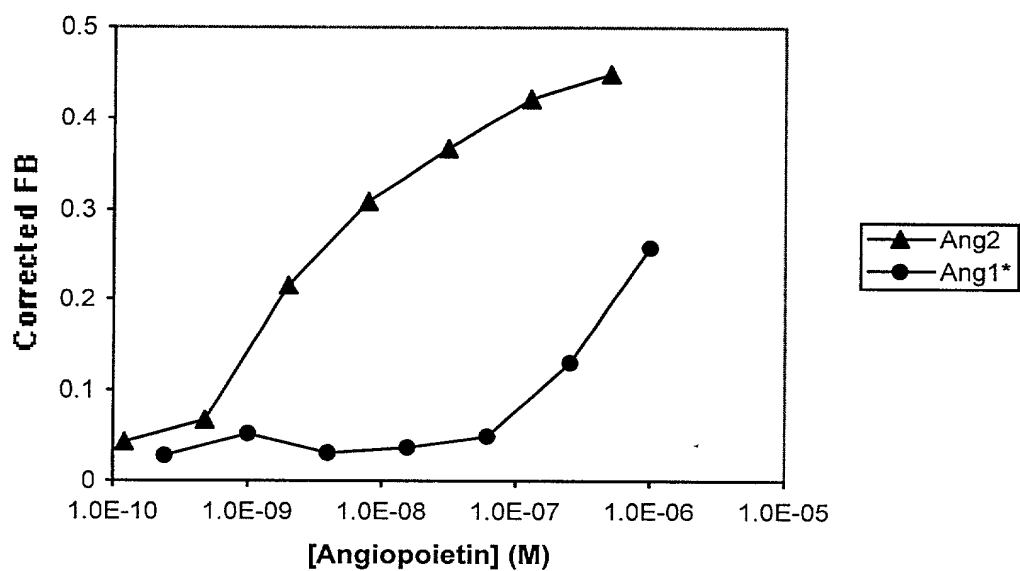
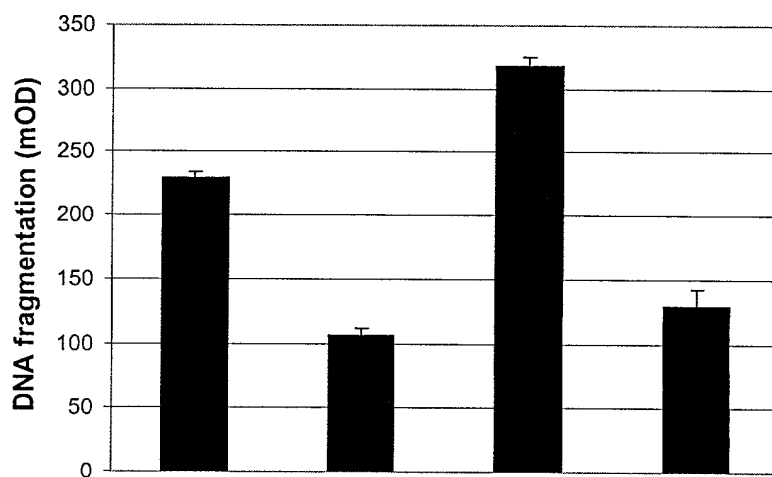


Figure 27



Ang2:

Fold-excess aptamer:

Aptamer:

-	+	+	+
0	0	10	10
none		11-1	control

Figure 28

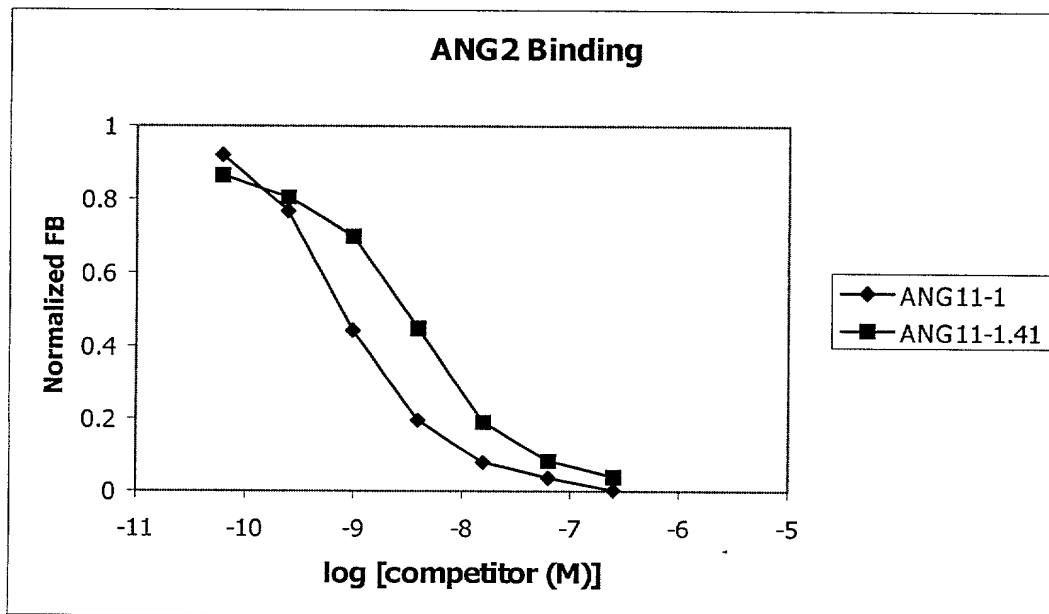
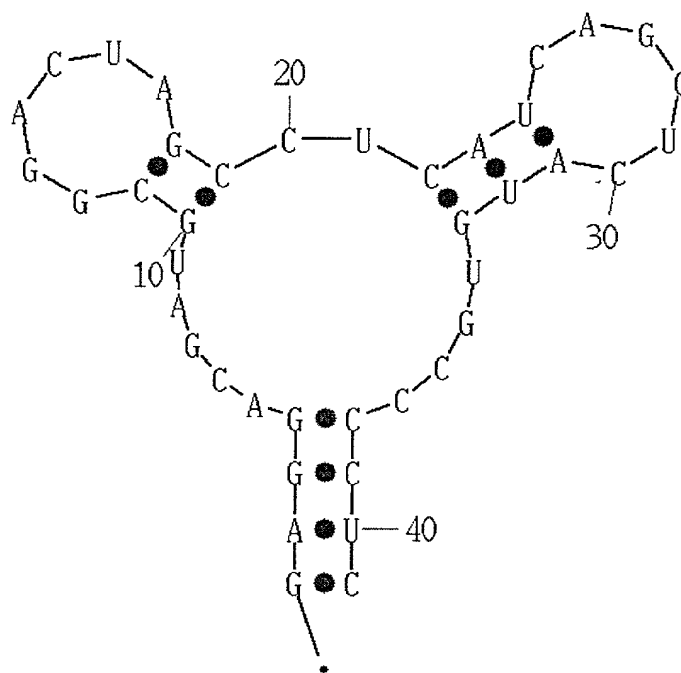


Figure 29

10960-233500

p1422.jpg by D. Stewart and M. Zuker  
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$dG = -1.43$  [initially  $-4.2$ ] ANG11-1.41

Figure 30

Figure 31

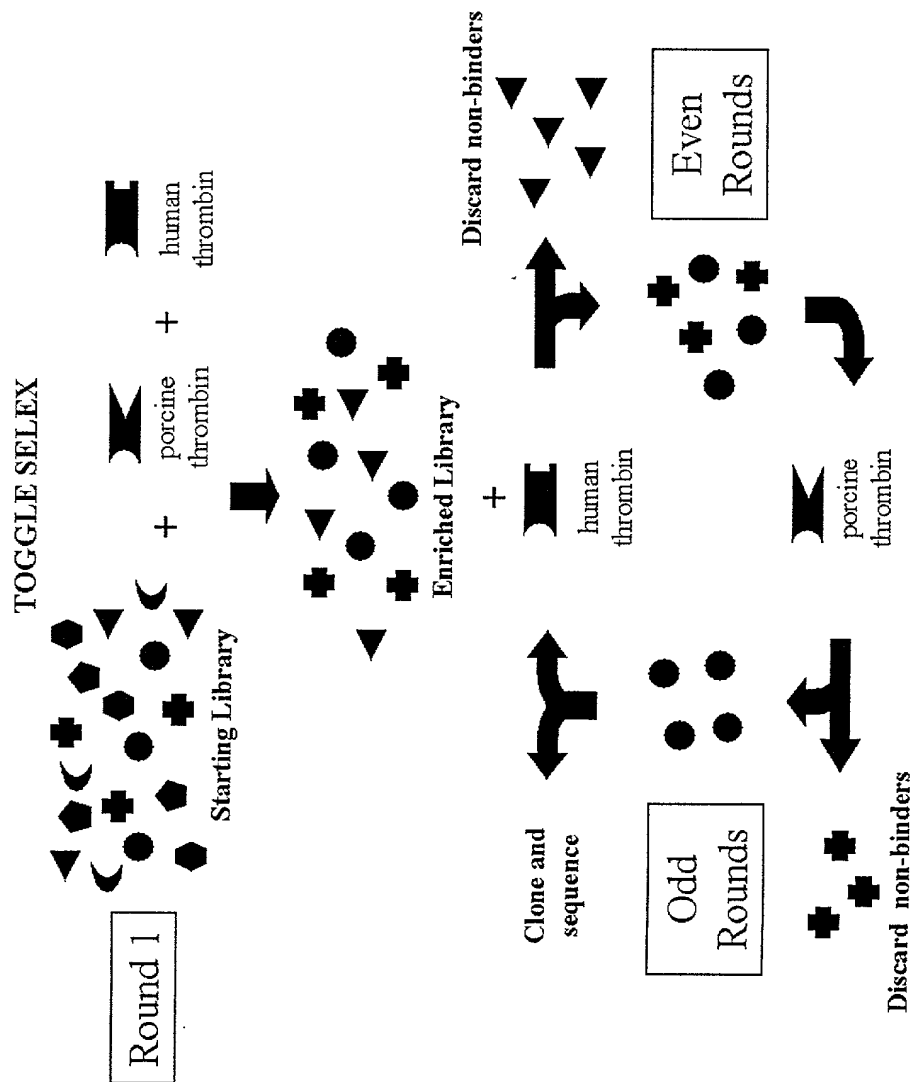


Figure 32

